



PCT09

H9

RAW SEQUENCE LISTING

DATE: 02/06/2002

PATENT APPLICATION: US/09/806,232B

TIME: 14:16:43

Input Set : A:\1241.18 Sequence Listing.txt

Output Set: N:\CRF3\02062002\I806232B.raw

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3 <110> APPLICANT: Seiki Motoharu
5 <120> TITLE OF INVENTION: DNA CODING FOR NOVEL POLYPEPTIDE
7 <130> FILE REFERENCE: 1241.18
9 <140> CURRENT APPLICATION NUMBER: US 09/806,232B
C--> 10 <141> CURRENT FILING DATE: 2001-11-29
12 <150> PRIOR APPLICATION NUMBER: PCT/JP99/05349
13 <151> PRIOR FILING DATE: 1999-09-29
15 <150> PRIOR APPLICATION NUMBER: JP10-276258
16 <151> PRIOR FILING DATE: 1998-09-29
18 <150> PRIOR APPLICATION NUMBER: JP10-291505
19 <151> PRIOR FILING DATE: 1998-09-29
21 <160> NUMBER OF SEQ ID NOS: 22
23 <170> SOFTWARE: PatentIn Ver. 2.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 587
27 <212> TYPE: PRT
28 <213> ORGANISM: Mouse
30 <400> SEQUENCE: 1
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32 1 5 10 15
34 Pro Arg Pro Gly Pro Gly Leu Pro Pro Leu Leu Leu Val Leu Ala Leu
35 20 25 30
37 Ala Ala His Gly Gly Cys Ala Ala Pro Ala Pro Arg Ala Glu Asp Leu
38 35 40 45
40 Ser Leu Gly Val Glu Trp Leu Ser Arg Phe Gly Tyr Leu Pro Pro Ala
41 50 55 60
43 Asp Pro Ala Ser Gly Gln Leu Gln Thr Gln Glu Glu Leu Ser Lys Ala
44 65 70 75 80
46 Ile Thr Ala Met Gln Gln Phe Gly Gly Leu Glu Thr Thr Gly Ile Leu
47 85 90 95
49 Asp Glu Ala Thr Leu Ala Leu Met Lys Thr Pro Arg Cys Ser Leu Pro
50 100 105 110
52 Asp Leu Pro Pro Gly Ala Gln Ser Arg Arg Lys Arg Gln Thr Pro Pro
53 115 120 125
55 Pro Thr Lys Trp Ser Lys Arg Asn Leu Ser Trp Arg Val Arg Thr Phe
56 130 135 140
58 Pro Arg Asp Ser Pro Leu Gly Arg Asp Thr Val Arg Ala Leu Met Tyr
59 145 150 155 160
61 Tyr Ala Leu Lys Val Trp Ser Asp Ile Thr Pro Leu Asn Phe His Glu
62 165 170 175
64 Val Ala Gly Asn Ala Ala Asp Ile Gln Ile Asp Phe Ser Lys Ala Asp
65 180 185 190
67 His Asn Asp Gly Tyr Pro Phe Asp Gly Pro Gly Gly Thr Val Ala His

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68          195          200          205
70 Ala Phe Phe Pro Gly Asp His His Thr Ala Gly Asp Thr His Phe Asp
71      210          215          220
73 Asp Asp Glu Pro Trp Thr Phe Arg Ser Ser Asp Ala His Gly Met Asp
74 225          230          235          240
76 Leu Phe Ala Val Ala Val His Glu Phe Gly His Ala Ile Gly Leu Ser
77          245          250          255
79 His Val Ala Ala Pro Ser Ser Ile Met Gln Pro Tyr Tyr Gln Gly Pro
80          260          265          270
82 Val Gly Asp Pro Val Arg Tyr Gly Leu Pro Tyr Glu Asp Arg Val Arg
83      275          280          285
85 Val Trp Gln Leu Tyr Gly Val Arg Glu Ser Val Ser Pro Thr Ala Gln
86      290          295          300
88 Leu Asp Thr Pro Glu Pro Glu Glu Pro Pro Leu Leu Pro Glu Pro Pro
89 305          310          315          320
91 Asn Asn Arg Ser Ser Thr Pro Pro Gln Lys Asp Val Pro His Arg Cys
92          325          330          335
94 Thr Ala His Phe Asp Ala Val Ala Gln Ile Arg Gly Glu Ala Phe Phe
95          340          345          350
97 Phe Lys Gly Lys Tyr Phe Trp Arg Leu Thr Arg Asp Arg His Leu Val
98      355          360          365
100 Ser Leu Gln Pro Ala Gln Met His Arg Phe Trp Arg Gly Leu Pro Leu
101      370          375          380
103 His Leu Asp Ser Val Asp Ala Val Tyr Glu Arg Thr Ser Asp His Lys
104 385          390          395          400
106 Ile Val Phe Phe Lys Gly Asp Arg Tyr Trp Val Phe Lys Asp Asn Asn
107          405          410          415
109 Val Glu Glu Gly Tyr Pro Arg Pro Val Ser Asp Phe Ser Leu Pro Pro
110          420          425          430
112 Gly Gly Ile Asp Ala Val Phe Ser Trp Ala His Asn Asp Arg Thr Tyr
113          435          440          445
115 Phe Phe Lys Asp Gln Leu Tyr Trp Arg Tyr Asp Asp His Thr Arg Arg
116      450          455          460
118 Met Asp Pro Gly Tyr Pro Ala Gln Gly Pro Leu Trp Arg Gly Val Pro
119 465          470          475          480
121 Ser Met Leu Asp Asp Ala Met Arg Trp Ser Asp Gly Ala Ser Tyr Phe
122          485          490          495
124 Phe Arg Gly Gln Glu Tyr Trp Lys Val Leu Asp Gly Glu Leu Glu Ala
125          500          505          510
127 Ala Pro Gly Tyr Pro Gln Ser Thr Ala Arg Asp Trp Leu Val Cys Gly
128          515          520          525
130 Glu Pro Leu Ala Asp Ala Glu Asp Val Gly Pro Gly Pro Gln Gly Arg
131          530          535          540
133 Ser Gly Ala Gln Asp Gly Leu Ala Val Cys Ser Cys Thr Ser Asp Ala
134 545          550          555          560
136 His Arg Leu Ala Leu Pro Ser Leu Leu Leu Leu Thr Pro Leu Leu Trp
137          565          570          575
139 Gly Leu Trp Thr Ser Val Ser Ala Lys Ala Ser
140          580          585

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142 <210> SEQ ID NO: 2
143 <211> LENGTH: 606
144 <212> TYPE: PRT
145 <213> ORGANISM: Homo sapiens
147 <400> SEQUENCE: 2
148 Met Arg Arg Arg Ala Ala Arg Gly Pro Gly Pro Pro Pro Pro Gly Pro
149   1           5           10           15
151 Gly Leu Ser Arg Leu Pro Leu Leu Pro Leu Pro Leu Leu Leu Leu
152           20           25           30
154 Ala Leu Gly Thr Arg Gly Gly Cys Ala Ala Pro Glu Pro Ala Arg Arg
155           35           40           45
157 Ala Glu Asp Leu Ser Leu Gly Val Glu Trp Leu Ser Arg Phe Gly Tyr
158           50           55           60
160 Leu Pro Pro Ala Asp Pro Thr Thr Gly Gln Leu Gln Thr Gln Glu Glu
161   65           70           75           80
163 Leu Ser Lys Ala Ile Thr Ala Met Gln Gln Phe Gly Gly Leu Glu Ala
164           85           90           95
166 Thr Gly Ile Leu Asp Glu Ala Thr Leu Ala Leu Met Lys Thr Pro Arg
167           100          105          110
169 Cys Ser Leu Pro Asp Leu Pro Val Leu Thr Gln Ala Arg Arg Arg Arg
170           115          120          125
172 Gln Ala Pro Ala Pro Thr Lys Trp Asn Lys Arg Asn Leu Ser Trp Arg
173           130          135          140
175 Val Arg Thr Phe Pro Arg Asp Ser Pro Leu Gly His Asp Thr Val Arg
176 145           150          155          160
178 Ala Leu Met Tyr Tyr Ala Leu Lys Val Trp Ser Asp Ile Ala Pro Leu
179           165          170          175
181 Asn Phe His Glu Val Ala Gly Ser Thr Ala Asp Ile Gln Ile Asp Phe
182           180          185          190
184 Ser Lys Ala Asp His Asn Asp Gly Tyr Pro Phe Asp Gly Pro Gly Gly
185           195          200          205
187 Thr Val Ala His Ala Phe Phe Pro Gly His His His Thr Ala Gly Asp
188           210          215          220
190 Thr His Phe Asp Asp Asp Glu Ala Trp Thr Phe Arg Ser Ser Asp Ala
191 225           230          235          240
193 His Gly Met Asp Leu Phe Ala Val Ala Val His Glu Phe Gly His Ala
194           245          250          255
196 Ile Gly Leu Ser His Val Ala Ala Ala His Ser Ile Met Arg Pro Tyr
197           260          265          270
199 Tyr Gln Gly Pro Val Gly Asp Pro Leu Arg Tyr Gly Leu Pro Tyr Glu
200           275          280          285
202 Asp Lys Val Arg Val Trp Gln Leu Tyr Gly Val Arg Glu Ser Val Ser
203           290          295          300
205 Pro Thr Ala Gln Pro Glu Glu Pro Pro Leu Leu Pro Glu Pro Pro Asp
206 305           310          315          320
208 Asn Arg Ser Ser Ala Pro Pro Arg Lys Asp Val Pro His Arg Cys Ser
209           325          330          335
211 Thr His Phe Asp Ala Val Ala Gln Ile Arg Gly Glu Ala Phe Phe Phe
212           340          345          350

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214 Lys Gly Lys Tyr Phe Trp Arg Leu Thr Arg Asp Arg His Leu Val Ser
215           355           360           365
217 Leu Gln Pro Ala Gln Met His Arg Phe Trp Arg Gly Leu Pro Leu His
218       370           375           380
220 Leu Asp Ser Val Asp Ala Val Tyr Glu Arg Thr Ser Asp His Lys Ile
221 385           390           395           400
223 Val Phe Phe Lys Gly Asp Arg Tyr Trp Val Phe Lys Asp Asn Asn Val
224           405           410           415
226 Glu Glu Gly Tyr Pro Arg Pro Val Ser Asp Phe Ser Leu Pro Pro Gly
227           420           425           430
229 Gly Ile Asp Ala Ala Phe Ser Trp Ala His Asn Asp Arg Thr Tyr Phe
230       435           440           445
232 Phe Lys Asp Gln Leu Tyr Trp Arg Tyr Asp Asp His Thr Arg His Met
233       450           455           460
235 Asp Pro Gly Tyr Pro Ala Gln Ser Pro Leu Trp Arg Gly Val Pro Ser
236 465           470           475           480
238 Thr Leu Asp Asp Ala Met Arg Trp Ser Asp Gly Ala Ser Tyr Phe Phe
239           485           490           495
241 Arg Gly Gln Glu Tyr Trp Lys Val Leu Asp Gly Glu Leu Glu Val Ala
242           500           505           510
244 Pro Gly Tyr Pro Gln Ser Thr Ala Arg Asp Trp Leu Val Cys Gly Asp
245       515           520           525
247 Ser Gln Ala Asp Gly Ser Val Ala Ala Gly Val Asp Ala Ala Glu Gly
248       530           535           540
250 Pro Arg Ala Pro Pro Gly Gln His Asp Gln Ser Arg Ser Glu Asp Gly
251 545           550           555           560
253 Tyr Glu Val Cys Ser Cys Thr Ser Gly Ala Ser Ser Pro Pro Gly Ala
254           565           570           575
256 Pro Gly Pro Leu Val Ala Ala Thr Met Leu Leu Leu Leu Pro Pro Leu
257           580           585           590
259 Ser Pro Gly Ala Leu Trp Thr Ala Ala Gln Ala Leu Thr Leu
260       595           600           605
262 <210> SEQ ID NO: 3
263 <211> LENGTH: 3517
264 <212> TYPE: DNA
265 <213> ORGANISM: Mouse
267 <220> FEATURE:
268 <221> NAME/KEY: CDS
269 <222> LOCATION: (86)..(1846)
271 <400> SEQUENCE: 3
272 ggcacgaggg cgcgagccg agcgaggcgc ggagctggct gctggcgggt gcggggaccc 60
274 tcgccacccg acctgggaga gcggg atg gga cgc cgc ccg cgg gga cct ggg 112
275           Met Gly Arg Arg Pro Arg Gly Pro Gly
276           1           5
278 tcc ccc cgg gga cct ggc cct cca cgc ccc ggg ccg ggg ctg cca cca 160
279 Ser Pro Arg Gly Pro Gly Pro Pro Arg Pro Gly Pro Gly Leu Pro Pro
280 10           15           20           25
282 ctg ctg ctt gta ctg gcg ctg gcg gcc cat ggg ggc tgc gca gcg ccc 208
283 Leu Leu Leu Val Leu Ala Leu Ala Ala His Gly Gly Cys Ala Ala Pro

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284		30		35		40		
286	gcg ccc cgc	gag gac ctc	agc ctc	gtg gag tgg	cta agc	agg	256	
287	Ala Pro Arg	Ala Glu Asp	Leu Ser	Leu Gly Val	Glu Trp	Leu Ser Arg		
288		45		50		55		
290	ttt ggc tac	ctg ccg cct	gca gat	ccg gca tca	ggg cag	cta cag acc	304	
291	Phe Gly Tyr	Leu Pro Pro	Ala Asp	Pro Ala Ser	Gly Gln	Leu Gln Thr		
292		60		65		70		
294	cag gag gaa	ctg tcc aaa	gcg att	act gcc atg	cag cag	ttt ggt ggt	352	
295	Gln Glu Glu	Leu Ser Lys	Ala Ile	Thr Ala Met	Gln Gln	Phe Gly Gly		
296		75		80		85		
298	ctg gag acc	act ggc atc	cta gat	gag gcc act	ctg gcc	ctg atg aaa	400	
299	Leu Glu Thr	Thr Gly Ile	Leu Asp	Glu Ala Thr	Leu Ala	Leu Met Lys		
300	90		95		100		105	
302	acc cct cga	tgc tcc ctt	ccg gac	ctg ccc cct	ggg gcc	caa tcy aga	448	
303	Thr Pro Arg	Cys Ser Leu	Pro Asp	Leu Pro Pro	Gly Ala	Gln Ser Arg		
304		110		115		120		
306	agg aag cgg	cag act cca	ccc cca	acc aaa	tgg agc	aag agg aac ctt	496	
307	Arg Lys Arg	Gln Thr Pro	Pro Pro	Thr Lys Trp	Ser Lys	Arg Asn Leu		
308		125		130		135		
310	tct tgg agg	gtc cgg aca	ttc cca	cgg gac tca	ccc ctg	ggc cgg gat	544	
311	Ser Trp Arg	Val Arg Thr	Phe Pro	Arg Asp Ser	Pro Leu	Gly Arg Asp		
312		140		145		150		
314	act gtg cgt	gca ctc atg	tac tac	gcc ctc	aaa gtc	tgg agt gac atc	592	
315	Thr Val Arg	Ala Leu Met	Tyr Tyr	Ala Leu Lys	Val Trp	Ser Asp Ile		
316		155		160		165		
318	aca ccc ttg	aac ttc cac	gag gta	gcg ggc	aac gcg	gcg gac atc cag	640	
319	Thr Pro Leu	Asn Phe His	Glu Val	Ala Gly Asn	Ala Ala	Asp Ile Gln		
320	170		175		180		185	
322	atc gac ttc	tcc aag gcc	gac cac	aat gac	ggc tac	ccc ttc gat ggc	688	
323	Ile Asp Phe	Ser Lys Ala	Asp His	Asn Asp	Gly Tyr	Pro Phe Asp Gly		
324		190		195		200		
326	cct ggt ggc	acg gtg gcc	cac gca	ttc ttc	cct ggt	gac cac cac acg	736	
327	Pro Gly Gly	Thr Val Ala	His Ala	Phe Phe	Pro Gly	Asp His His Thr		
328		205		210		215		
330	gca ggg gac	acc cac ttt	gat gac	gat gag	cca tgg	acc ttc cgt tcc	784	
331	Ala Gly Asp	Thr His Phe	Asp Asp	Asp Glu	Pro Trp	Thr Phe Arg Ser		
332		220		225		230		
334	tca gat gcc	cac ggg atg	gac ctg	ttt gca	gtg gcc	gtc cat gag ttt	832	
335	Ser Asp Ala	His Gly Met	Asp Leu	Phe Ala	Val Ala	Val His Glu Phe		
336		235		240		245		
338	ggt cat gcc	att ggt ctg	agc cat	gtt gcc	gcc cca	agc tcc atc atg	880	
339	Gly His Ala	Ile Gly Leu	Ser His	Val Ala	Ala Pro	Ser Ser Ile Met		
340	250		255		260		265	
342	caa ccg tac	tac cag ggc	ccc gtg	ggt gac	ccc gta	cgc tat gga ctt	928	
343	Gln Pro Tyr	Tyr Gln Gly	Pro Val	Gly Asp	Pro Val	Arg Tyr Gly Leu		
344		270		275		280		
346	ccc tat gag	gac agg gtg	cgt gtc	tgg cag	ttg tac	ggt gtg cgg gaa	976	
347	Pro Tyr Glu	Asp Arg Val	Arg Val	Trp Gln	Leu Tyr	Gly Val Arg Glu		
348		285		290		295		

VERIFICATION SUMMARY

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Input Set : A:\1241.18 Sequence Listing.txt

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date